AMENDMENTS TO THE CLAIMS

Please amend the claims as follows.

Please cancel claims 3, 4, 7-10, 17-28, 30-46, 93, 94, 108-110, and 116, without prejudice.

1. (currently amended) An isolated or recombinant nucleic acid comprising (a) a sequence ~~that encodes a polypeptide having alpha amylase activity, wherein said sequence~~ having at least about 70% sequence identity to a sequence as set forth in ~~is selected from the group consisting of: SEQ ID NO: 1; variants having at least about 50% homology to at least one of~~ SEQ ID NO:1, over a region of at least about 100 residues, wherein the nucleic acid encodes a polypeptide having alpha amylase activity, ~~as determined by analysis with a sequence comparison algorithm or by visual inspection~~; and (b) sequences complementary to (a) ~~to SEQ ID NO: 1; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~.

2. (currently amended) An [[The]] isolated or recombinant nucleic acid comprising (a) a ~~as claimed in claim 1, wherein the isolated nucleic acid comprises a complementary~~ sequence encoding a polypeptide having alpha amylase activity, wherein said sequence [[that]] hybridizes under conditions of high stringency to a sequence selected from the group consisting of: SEQ ID NO:1, and (b) sequences complementary to (a) ~~variants having at least about 50% homology to at least one of SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~, wherein the conditions of high stringency comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution.

3-4. (canceled)

5. (currently amended) The isolated or recombinant nucleic acid of ~~as claimed in~~ claim 1, wherein said sequence has at least about 70% sequence identity to a sequence as set forth in ~~variants have at least about 50% homology to at least one of~~ SEQ ID NO:1, over a region of at least about 200 residues~~, as determined by analysis with a sequence comparison algorithm~~.

6. (currently amended) The isolated or recombinant nucleic acid of ~~as claimed in~~ claim 1, wherein said sequence has at least about 70% sequence identity to a sequence as set forth in ~~variants have at least about 50% homology to at least one of~~ SEQ ID NO:1 over the entire sequence.

7-10. (canceled)

11. (currently amended) The isolated or recombinant nucleic acid of ~~according to~~ claim 1, ~~2, 3, 4, 5 or 6,~~ wherein said sequence has ~~variants have~~ at least about 75% sequence identity to a sequence as set forth in ~~homology to at least one of~~ SEQ ID NO:1.

12. (currently amended) The isolated or recombinant nucleic acid of ~~according to~~ claim 1, ~~2, 3, 4, 5 or 6,~~ wherein said sequence has ~~variants have~~ at least about 80% sequence identity to a sequence as set forth in ~~homology to at least one of~~ SEQ ID NO:1.

13. (currently amended) The isolated or recombinant nucleic acid of ~~according to~~ claim 1, ~~2, 3, 4, 5 or 6,~~ wherein said sequence has ~~variants have~~ at least about 85% sequence identity to a sequence as set forth in ~~homology to at least one of~~ SEQ ID NO:1.

14. (currently amended) The isolated or recombinant nucleic acid of ~~according to~~ claim 1, ~~2, 3, 4, 5 or 6,~~ wherein said sequence has ~~variants have~~ at least about 90% sequence identity to a sequence as set forth in ~~homology to at least one of~~ SEQ ID NO:1.

15. (currently amended) The isolated or recombinant nucleic acid of ~~according to~~ claim 1, ~~2, 3, 4, 5 or 6,~~ wherein said sequence has ~~variants have~~ at least about 95% sequence identity to a sequence as set forth in ~~homology to at least one of~~ SEQ ID NO:1.

16. (currently amended) The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is determined using a sequence comparison algorithm comprising [[is]] FASTA version 3.0t78 with the default parameters.

17-28. (canceled)

29. (currently amended) An isolated or recombinant nucleic acid encoding a polypeptide ~~selected from the group consisting of: polypeptides~~ having an amino acid sequence ~~selected from the group consisting of: SEQ ID NO: 2; variants~~ having at least about 70% sequence identity to a sequence as set forth in ~~50% homology to at least one of~~ SEQ ID NO: 2, over a region of at least about 100 residues~~, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 2; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO: 2~~.

30-46. (canceled)

47. (currently amended) A method of producing a polypeptide ~~selected from the group consisting of: polypeptides having an amino acid sequence selected from the group consisting of: SEQ ID NO: 2; variants having at least about 50% homology to at least one of SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 2; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 2 over a region of~~

~~at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and polypeptides having at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NO: 2;~~ comprising the steps of introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide, wherein the nucleic acid comprises the sequence of claim 1 or claim 2 ~~and recovering the polypeptide~~.

48. (currently amended) A method of producing a polypeptide ~~comprising at least 10 amino acids of a sequence selected from the group consisting of SEQ ID NO: 2,~~ comprising the steps of: introducing a nucleic acid as set forth in claim 1 or claim 2 ~~encoding the polypeptide,~~ operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide, and recovering the polypeptide.

49. (currently amended) A method of generating a variant comprising: obtaining a nucleic acid as set forth in claim 1 or claim 2 ~~comprising a polynucleotide selected from the group consisting of: SEQ ID NO: 1; variants having at least about 50% homology to at least one of SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 1; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and fragments comprising at least 30 consecutive nucleotides any of the foregoing sequences;~~ and modifying one or more nucleotides in said polynucleotide to another nucleotide, deleting one or more nucleotides in said polynucleotide, or adding one or more nucleotides to said polynucleotide.

50. (currently amended) The method of claim 49, wherein the modifications are introduced by a method selected from the group consisting of: error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble

mutagenesis, site-specific mutagenesis, gene reassembly, ~~gene site saturated mutagenesis~~ Gene Site Saturation Mutagenesis™ (GSSM™) and any combination of these methods.

51. (withdrawn) The method of claim 50, wherein the modifications are introduced by error-prone PCR.

52. (withdrawn) The method of claim 50, wherein the modifications are introduced by shuffling.

53. (withdrawn) The method of claim 50, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

54. (withdrawn) The method of claim 50, wherein the modifications are introduced by assembly PCR.

55. (withdrawn) The method of claim 50, wherein the modifications are introduced by sexual PCR mutagenesis.

56. (withdrawn) The method of claim 50, wherein the modifications are introduced by *in vivo* mutagenesis.

57. (withdrawn) The method of claim 50, wherein the modifications are introduced by cassette mutagenesis.

58. (withdrawn) The method of claim 50, wherein the modifications are introduced by recursive ensemble mutagenesis.

59. (withdrawn) The method of claim 50, wherein the modifications are introduced by exponential ensemble mutagenesis.

60. (withdrawn) The method of claim 50, wherein the modifications are introduced by site-specific mutagenesis.

61. (withdrawn) The method of claim 50, wherein the modifications are introduced by gene reassembly.

62. (currently amended) The method of claim 50, wherein the modifications are introduced by ~~gene site saturated mutagenesis~~ Gene Site Saturation Mutagenesis™ (GSSM™).

63. (currently amended) A computer readable medium having stored thereon a sequence as set forth in claim 1 or claim 2 ~~selected from the group consisting of: nucleic acid sequences of SEQ ID NO: 1; variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; nucleic acid sequences complementary to SEQ ID NO: 1; nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences SEQ ID NO: 2; variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences complementary to SEQ ID NO: 2; and polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~.

64. (currently amended) A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence as set forth in claim 1 or claim 2 ~~selected from the group consisting of: nucleic acid sequences of SEQ ID NO: 1; variants~~

~~of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; nucleic acid sequences complementary to SEQ ID NO: 1; nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences SEQ ID NO: 2; variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences complementary to SEQ ID NO: 2; and polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.~~

65. (withdrawn) The computer system of claim 64, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

66. (withdrawn) The computer system of claim 65, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

67. (withdrawn) The computer system of claim 64, further comprising an identifier which identifies one or more features in said sequence.

68. (currently amended) A method for comparing a first sequence to a second sequence comprising the steps of: reading the first sequence and the second sequence through use of a computer program which compares sequences; and determining differences between the first sequence and the second sequence with the computer program, wherein said first sequence comprises [[is]] a sequence as set forth in claim 1 or claim 2 ~~selected from the group consisting of: nucleic acid sequences of SEQ ID NO: 1; variants of a nucleic acid sequence having at least about~~

~~50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; nucleic acid sequences complementary to SEQ ID NO: 1; nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences SEQ ID NO: 2; variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences complementary to SEQ ID NO: 2; and polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~.

69. (withdrawn) The method of claim 68, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

70. (currently amended) A method for identifying a feature in a sequence comprising the steps of: reading the sequence using a computer program which identifies one or more features in a sequence; and identifying one or more features in the sequence with the computer program, wherein the sequence comprises [[is]] a sequence as set forth in claim 1 or claim 2 ~~is selected from the group consisting of: nucleic acid sequences of SEQ ID NO: 1; variants of a nucleic acid sequence having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; nucleic acid sequences complementary to SEQ ID NO: 1; nucleic acid sequences complementary to variants of nucleic acid sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences SEQ ID NO: 2; variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID~~

~~NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences complementary to SEQ ID NO: 2; and polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~.

71. (currently amended) A method of hydrolyzing a starch linkage comprising contacting a substance comprising ~~containing~~ the starch with a polypeptide encoded by the nucleic acid of claim 1 or claim 2 ~~selected from the group consisting of SEQ ID NO: 2, and sequences substantially identical thereto~~, under conditions which facilitate the hydrolysis of the starch ~~carbon-halogen linkage~~.

72. (currently amended) A method of catalyzing the breakdown of a starch, comprising the step of contacting a sample comprising ~~containing~~ starch with a polypeptide encoded by the nucleic acid of claim 1 or claim 2 ~~having a sequence selected from the group consisting of: polypeptide sequences SEQ ID NO: 2; variants of polypeptide sequences having at least about 50% homology to at least one of SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; polypeptide sequences complementary to SEQ ID NO: 2; and polypeptide sequences complementary to variants of polypeptide sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~; under conditions which facilitate the breakdown of the starch ~~haloalkane or halocarboxylic acid~~.

73. (currently amended) An assay for identifying a ~~functional~~ polypeptide having alpha amylase activity, wherein the polypeptide is ~~fragments or variants~~ encoded by a subsequence ~~fragments~~ of the nucleic acid of claim 1 or claim 2 ~~SEQ ID NO: 1, and sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, which retain at least one~~

~~property of the polypeptides of SEQ ID NO: 2, and sequences having at least about 50% homology to SEQ ID NO: 2, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection,~~ said assay comprising the steps of:

contacting the polypeptide ~~of SEQ ID NO: 2, and sequences having at least about 50% homology to SEQ ID NO: 2 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, polypeptide fragments or variants encoded by SEQ ID NO: 1, sequences having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and sequences complementary to any of the foregoing sequences~~ with a substrate molecule under conditions which allow the ~~particular~~ polypeptide to function as an alpha amylase; and

(b) detecting either a decrease in an amount of a substrate or an increase in an amount of a reaction product which results from a reaction between said polypeptide and said substrate; wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product identifies a ~~is indicative of existence of the~~ functional polypeptide.

74. (currently amended) A nucleic acid probe comprising an oligonucleotide at least [[from]] about 10 [[to 50]] nucleotides in length and having a segment of at least 10 contiguous nucleotides complementary to a subsequence of the nucleic acid of claim 1 or claim 2 ~~that is at least 50% complementary to a nucleic acid target region of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1~~; and which hybridizes to the nucleic acid of claim 1 or claim 2 ~~target region~~ under ~~moderate to highly~~ stringent conditions to form a detectable target:probe duplex.

75. (currently amended) The probe of claim 74, wherein the oligonucleotide comprises [[is]] DNA or RNA.

76. (currently amended) The probe of claim 74, wherein the oligonucleotide has a segment of at least [[10]] 15 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 55% complementary to the nucleic acid target region~~.

77. (currently amended) The probe of claim [[74]] 76, wherein the oligonucleotide has a segment of at least [[10]] 20 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 60% complementary to the nucleic acid target region~~.

78. (currently amended) The probe of claim [[74]] 77, wherein the oligonucleotide has a segment of at least [[10]] 25 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 65% complementary to the nucleic acid target region~~.

79. (currently amended) The probe of claim [[74]] 78, wherein the oligonucleotide has a segment of at least [[10]] 30 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 70% complementary to the nucleic acid target region~~.

80. (currently amended) The probe of claim [[74]] 79, wherein the oligonucleotide has a segment of at least [[10]] 35 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~.

81. (currently amended) The probe of claim [[74]] 80, wherein the oligonucleotide has a segment of at least [[10]] 40 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~.

82. (currently amended) The probe of claim [[74]] 81, wherein the oligonucleotide has a segment of at least [[10]] 50 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~.

83. (currently amended) The probe of claim [[74]] 82, wherein the oligonucleotide has a segment of at least [[10]] 75 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~

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84. (currently amended) The probe of claim [[74]] 83, wherein the oligonucleotide has a segment of at least [[10]] 100 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~.

85. (currently amended) The probe of claim [[74]] 84, wherein the oligonucleotide has a segment of at least [[10]] 150 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~that is at least 75% complementary to the nucleic acid target region~~.

86. (original) The probe of claim 74, wherein the oligonucleotide is 15-50 bases in length.

87. (currently amended) The probe of claim 74, wherein the probe further comprises a detectable isotopic label or a detectable non-isotopic label.

88. (currently amended) The probe of claim [[74]] 84, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.

89. (currently amended) The probe of claim 86, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides [[that is]] having at least 90% sequence identity SEQ ID NO:1 or its complementary sequence ~~to the nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex~~.

90. (currently amended) The probe of claim [[86]] 89, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides [[that is]] having at least 95% sequence identity SEQ ID NO:1 or its complementary sequence ~~to the nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex~~.

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91. (currently amended) The probe of claim [[86]] 90, wherein the oligonucleotide has a segment of at least 15 contiguous nucleotides [[that is]] having at least 97% sequence identity SEQ ID NO:1 or its complementary sequence ~~to the nucleic acid target region, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex~~.

92. (currently amended) A polynucleotide probe for isolation or identification of alpha amylase genes having a sequence which is the same as, or fully complementary to at least 15 contiguous nucleotides of the nucleic acid of claim 1 or claim 2 ~~at least a fragment of one of SEQ ID NO: 1~~.

93-94. (canceled)

95. (currently amended) A method for modifying small molecules, comprising the step of mixing at least one polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~a polynucleotide selected from the group consisting of: SEQ ID NO: 1; variants having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 1; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and fragments of any of the foregoing polypeptides~~; with at least one small molecule to produce at least one modified small molecule via at least one biocatalytic reaction~~, wherein the at least one polypeptide has alpha amylase activity~~.

96. (withdrawn) The method of claim 95, wherein the at least one polypeptide comprises a plurality of polypeptides and the at least one small molecule comprises a plurality of

small molecules, whereby a plurality of modified small molecules are produced via a plurality of biocatalytic reactions to form a library of modified small molecules.

97. (withdrawn) The method of 96, further comprising the step of testing the library to determine if a particular modified small molecule, which exhibits a desired activity is present within the library.

98. (withdrawn) The method of claim 97 wherein the step of testing the library further comprises the steps of: systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with the desired activity, and identifying a specific biocatalytic reaction which produces the particular modified small molecule of desired activity.

99. (withdrawn) The method of claim 98 wherein the specific biocatalytic reaction, which produces the modified small molecule of desired activity is repeated.

100. (withdrawn) The method of claim 93 wherein the biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the at least one small molecule; each biocatalyst is specific for a particular structural moiety or a group of related structural moieties; and each biocatalyst reacts with a plurality of small molecules which contain the particular structural moiety specific to the particular biocatalyst.

101. (currently amended) A cloning vector comprising the nucleic acid of claim 1 or claim 2 ~~a sequence that encodes a polypeptide having alpha amylase activity, said sequence being selected from the group consisting of: SEQ ID NO: 1; variants having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 1; and sequences complementary to variants having at least about 50% homology to~~

~~SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.~~

102. (currently amended) A host cell comprising the nucleic acid of claim 1 or claim 2 ~~a sequence that encodes a polypeptide having alpha-amylase activity, said sequence being selected from the group consisting of: SEQ ID NO: 1; variants having at least about 50% homology to at least one of SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NO: 1; and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 1, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection~~.

103. (currently amended) An expression vector capable of replicating in a host cell comprising the nucleic acid of claim 1 or claim 2 ~~a polynucleotide having a sequence selected from the group consisting of SEQ ID NO: 1, variants having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NO: 1, and sequences complementary to variants having at least about 50% homology to SEQ ID NO: 1 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency~~.

104. (currently amended) A vector as claimed in claim 101 or 103, wherein the vector comprises ~~is selected from the group consisting of~~ a viral vector ~~vectors~~, a plasmid ~~vectors~~, a phage ~~vectors~~, a phagemid ~~vectors~~, a cosmids, a fosmid ~~fosmids~~, a bacteriophage ~~bacteriophages~~, an artificial chromosome ~~chromosomes~~, an adenovirus vector ~~vectors~~, a retroviral vector ~~vectors~~, [[and]] or an adeno-associated viral vector ~~vectors~~.

105. (currently amended) A host cell comprising the ~~an expression~~ vector of ~~as claimed in~~ claim 101 or 103.

106. (currently amended) The [[A]] host cell of ~~as claimed in~~ claim [[47,]] 102 [[, 103]] or claim 105, wherein the host cell is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and metabolically rich hosts.

107. (currently amended) A method for liquefying a starch-comprising ~~starch containing~~ composition comprising the step of contacting the starch with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~.

108-110. (canceled)

111. (currently amended) A method for washing an object comprising the step of contacting said object with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~ under conditions sufficient for said washing.

112. (currently amended) A method for textile desizing comprising the step of contacting said textile with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~ under conditions sufficient for said desizing.

113. (currently amended) A method for the treatment of lignocellulosic fibers comprising the step of contacting [[, wherein]] the fibers ~~are treated~~ with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~, in an amount effective ~~which is efficient~~ for improving a [[the]] fiber property ~~properties~~.

114. (currently amended) A method ~~according to claim 113~~ for enzymatic deinking of recycled paper pulp, ~~wherein~~ comprising the step of contacting the recycled paper pulp with a [[the]] polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2

~~of claim 30 is applied~~ in an amount ~~which is~~ efficient for effective deinking of the recycled paper pulp ~~fiber surface~~.

115. (currently amended) A method for starch liquefaction comprising contacting said starch with with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~ under conditions sufficient for said liquefaction.

116. (canceled)

117. (currently amended) The [[A]] method of claim 107 ~~as in any of claims 107-116~~, wherein the polypeptide having alpha amylase activity encoded by the nucleic acid has a sequence as [[is]] set forth in SEQ ID NO: 2~~, or functional variants thereof~~.

118. (currently amended) A method for producing a high-maltose or a high-glucose syrup or a mixed syrup comprising: liquefying starch using an effective amount of a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~ to obtain a soluble starch hydrolysate; and saccharifying the soluble starch hydrolysate, thereby resulting in a syrup.

119. (currently amended) The method ~~as in any~~ of ~~claims~~ claim 107, ~~115, or 118,~~ wherein the starch is from a material comprising ~~selected from~~ rice, germinated rice, corn, barley, wheat, legumes [[and]] or sweet potato.

120. (currently amended) The method ~~as in any~~ of ~~claims~~ claim 107, ~~115, or 118,~~ further comprising addition of a second alpha amylase or a beta amylase or a combination thereof.

121. (currently amended) A method of increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging fluid formed

during production operations and found within the subterranean formation which surrounds a completed well bore comprising:

allowing production fluids to flow from the well bore;

reducing the flow of production fluids from the formation below expected flow rates;

formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 ~~of claim 30~~;

pumping the enzyme treatment to a desired location within the well bore [[;]] and allowing the enzyme treatment to degrade the viscous, starch-containing, damaging fluid, such that ~~whereby~~ the enzyme-treated production fluid can be removed from the subterranean formation to the well surface~~; and wherein the enzyme treatment is effective to attack the alpha glucosidic linkages in the starch-containing fluid~~.

122. (currently amended) The method of claim 121, wherein the enzyme has a sequence as [[is]] set forth in SEQ ID NO: 2.

123. (new) An isolated or recombinant nucleic acid comprising (a) a sequence having at least about 90% sequence identity to SEQ ID NO:1, wherein the nucleic acid encodes a polypeptide having alpha amylase activity; and (b) a sequence complementary to (a).

124. (new) The isolated or recombinant nucleic acid of claim 123, wherein in (a) the sequence has at least about 95% sequence identity to SEQ ID NO:1.